



REPLACEMENT SHEET
Application No. 10/506,406, filed 3/14/05
Inventors: Swiercz et al.

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GAATTCCTGCAGCTCAGCAGCCGCCGAGAGCAGGACGAACCGCCAATCGCAAGGCACC
1  -----+-----+-----+-----+-----+-----+ 60
CTTAAGGACGTCGAGTCGTCGGCGGCGGTCTCGTCCTGCTTGGCGGTTAGCGTTCGTGG

TCTGAGAACTTCAGGATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCCTGGGCCTGGCC
61  -----+-----+-----+-----+-----+-----+ 120
AGACTCTTGAAGTCCTACGTCTACAGAGGTGCGGAGTGGACGGATCAGGACCCGGACCGG
aa      M Q M S P A L T C L V L G L A -
      |Signal Peptide
CTTGTCTTTGGTGAAGGTCTGCTGTGCACCATCCCCATCCTACGTGGCCACCTGGCC
121  -----+-----+-----+-----+-----+-----+ 180
GAACAGAAACCACTTCCCAGACGACACGTGGTAGGGGTAGGATGCACCGGGTGGACCGG
aa      L V F G E G S A |V H H P P S Y V A H L A 12
      |Start Mature Protein
TCAGACTTCGGGGTGAGGGTGTTTCAGCAGGTGGCGCAGGCCTCCAAGGACCGCAACGTG
181  -----+-----+-----+-----+-----+-----+ 240
AGTCTGAAGCCCCACTCCACAAAGTCGTCCACCGCGTCCGGAGGTTCTTGCGGTTGCAC
aa      S D F G V R V F Q Q V A Q A S K D R N V 32

GTTTTCTCACCTATGGGGTGGCCTCGGTGTTGGCCATGCTCCAGCTGACAACAGGAGGA
241  -----+-----+-----+-----+-----+-----+ 300
CAAAAGAGTGGGATACCCACCGGAGCCACAACCGGTACGAGGTCGACTGTTGTCCTCCT
aa      V F S P Y G V A S V L A M L Q L T T G G 52

GAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAAGGGCATGGCC
301  -----+-----+-----+-----+-----+-----+ 360
CTTTGGGTCGTCGTCTAAGTTCGTGATACCCTAAGTTCTAACTACTGTTCCCGTACCGG
aa      E T Q Q Q I Q A A M G F K I D D K G M A 72

CCCGCCCTCCGGCATCTGTACAAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGC
361  -----+-----+-----+-----+-----+-----+ 420
GGGCGGGAGGCCGTAGACATGTTCTCGAGTACCCCGGTACCTTGTTCTACTCTAGTCG
aa      P A L R H L Y K E L M G P W N K D E I S 92

ACCACAGACGCGATCTTCGTCCAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCAC
421  -----+-----+-----+-----+-----+-----+ 480
TGGTGTCTGCGCTAGAAGCAGGTGCGCCTAGACTTCGACCAGGTCCCGAAGTACGGGGTG
aa      T T D A I F V Q R D L K L V Q G F M P H 112

TTCTTCAGGCTGTTCCGGAGCACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCC
481  -----+-----+-----+-----+-----+-----+ 540
AAGAAGTCCGACAAGGCCTCGTGCCAGTTCGTTACCTGAAAAGTCTCCACCTCTCTCGG
aa      F F R L F R S T V K Q V D F S E V E R A 132
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FIG.1A

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AGATTCATCATCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGCAACTTGCTT
541 -----+-----+-----+-----+-----+-----+ 600
TCTAAGTAGTAGTTACTGACCCACTTCTGTGTGTGTTTTCCATACTAGTCGTTGAACGAA
aa R F I I N D W V K T H T K G M I S N L L 152

GGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGTGAATGCCCTCTACTTCAAC
601 -----+-----+-----+-----+-----+-----+ 660
CCCTTTCCTCGGCACCTGGTCGACTGTGCCGACCACGACCACTTACGGGAGATGAAGTTG
aa G K G A V D Q L T R L V L V N A L Y F N 172

GGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAAATCA
661 -----+-----+-----+-----+-----+-----+ 720
CCGGTCACCTTCTGAGGGAAGGGGCTGAGGTCTGCGGTGGCGCGGAGAAGGTGTTTAGT
aa G Q W K T P F P D S S T H R R L F H K S 192

GACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAG
721 -----+-----+-----+-----+-----+-----+ 780
CTGCCGTCGTGACAGAGACACGGGTACTACCGAGTCTGGTTGTTCAAGTTGATATGACTC
aa D G S T V S V P M M A Q T N K F N Y T E 212

TTCACCACGCCCCGATGGCCATTACTACGACATCCTGGAAGTGCCTACCCACGGGGACACC
781 -----+-----+-----+-----+-----+-----+ 840
AAGTGGTGCGGGCTACCGGTAATGATGCTGTAGGACCTTGACGGGATGGTGCCCTGTGG
aa F T T P D G H Y Y D I L E L P Y H G D T 232

CTCAGCATGTTCAATTGCTGCCCTTATGAAAAAGAGGTGCCTCTCTCTGCCCTCACCAAC
841 -----+-----+-----+-----+-----+-----+ 900
GAGTCGTACAAGTAACGACGGGGAATACTTTTTCTCCACGGAGAGAGACGGGAGTGGTTG
aa L S M F I A A P Y E K E V P L S A L T N 252

ATTCTGAGTGCCCAGCTCATCAGCCACTGGAAAGGCAACATGACCAGGCTGCCCCGCCTC
901 -----+-----+-----+-----+-----+-----+ 960
TAAGACTCACGGGTCGAGTAGTCGGTGACCTTTCGTTGTACTGGTCCGACGGGGCGGAG
aa I L S A Q L I S H W K G N M T R L P R L 272

CTGGTTCTGCCAAGTTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCCCTAGAGAAC
961 -----+-----+-----+-----+-----+-----+ 1020
GACCAAGACGGGTTCAAGAGGGACCTCTGACTTCAGCTGGAGTCCTTCGGGGATCTCTTG
aa L V L P K F S L E T E V D L R K P L E N 292

CTGGGAATGACCGACATGTTTCAGACAGTTTCAGGCTGACTTCACGAGTCTTTCAGACCAA
1021 -----+-----+-----+-----+-----+-----+ 1080
GACCTTACTGGCTGTACAAGTCTGTCAAAGTCCGACTGAAGTGCTCAGAAAGTCTGGTT
aa L G M T D M F R Q F Q A D F T S L S D Q 312

FIG.1B

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1081  GAGCCTCTCCACGTCGCGCAGGCGCTGCAGAAAGTGAAGATCGAGGTGAACGAGAGTGGC
      -----+-----+-----+-----+-----+-----+ 1140
      CTCGGAGAGGTGCAGCGCGTCCGCGACGTCTTTCACCTTAGCTCCACTTGCTCTCACCG
aa    E P L H V A Q A L Q K V K I E V N E S G 332

1141  ACGGTGGCCTCCTCATCCACAGCTGTCTAGTCTCAGCCCGCATGGCCCCGAGGAGATC
      -----+-----+-----+-----+-----+-----+ 1200
      TGCCACCGGAGGAGTAGGTGTGACAGTATCAGAGTCGGGCGTACCGGGGGCTCCTCTAG
aa    T V A S S S T A V I V S A R M A P E E I 352

1201  ATCATGGACAGACCCTTCCTCTTTGTGGTCCGGCACAACCCACAGGAACAGTCCTTTTC
      -----+-----+-----+-----+-----+-----+ 1260
      TAGTACCTGTCTGGGAAGGAGAAACACCAGGCCGTGTTGGGGTGTCTTGTGAGGAAAAG
aa    I M D R P F L F V V R H N P T G T V L F 352

1261  ATGGGCCAAGTGATGGAACCCTGACCCTGGGGAAGACGCCTTCATCTGGGACAAAAGT
      -----+-----+-----+-----+-----+-----+ 1320
      TACCCGGTTCACTACCTGGGACTGGGACCCCTTTCTGCGGAAGTAGACCCTGTTTGTAC
aa    M G Q V M E P * 379

1321  GAGATGCATCGGGAAAGAAGAACTCCGAAGAAAAGAATTTTAGTGTTAATGACTCTTTC
      -----+-----+-----+-----+-----+-----+ 1380
      CTCTACGTAGCCCTTTCTTCTTTGAGGCTTCTTTCTTAAATCACAATTACTGAGAAAAG

1381  TGAAGGAAGAGAAGACATTTGCCTTTTGTAAAAGATGGTAAACCAGATCTGTCTCCAAG
      -----+-----+-----+-----+-----+-----+ 1440
      ACTTCCTTCTCTTCTGTAAACGGAAAACAATTTTCTACCATTGTTGCTAGACAGAGGTTT

1441  ACCTTGGCCTCTCCTTGGAGGACCTTTAGGTCAAACCTCCTAGTCTCCACCTGAGACCCT
      -----+-----+-----+-----+-----+-----+ 1500
      TGGAACCGGAGAGGAACCTCCTGGAATCCAGTTTGAGGGATCAGAGGTGGACTCTGGGA

1501  GGGAGAGAAGTTTGAAGCACAACCTCCCTTAAGGTCTCAAACCAGACGGTGACGCCTGCG
      -----+-----+-----+-----+-----+-----+ 1560
      CCCTCTCTTCAAACCTTCGTGTTGAGGGAATTCCAGAGGTTTGGTCTGCCACTGCGGACGC

1561  GGACCATCTGGGGCACCTGCTTCCACCCGTCTCTCTGCCCACTCGGGTCTGCAGACCTGG
      -----+-----+-----+-----+-----+-----+ 1620
      CCTGGTAGACCCCGTGGACGAAGGTGGGCAGAGAGACGGGTGAGCCAGACGTCTGGACC

1621  TTCCCACTGAGGCCCTTTGCAGGATGGAACCTACGGGGCTTACAGGAGCTTTTGTGTGCCT
      -----+-----+-----+-----+-----+-----+ 1680
      AAGGGTGACTCCGGGAAACGTCTACCTTGATGCCCCGAATGTCTCGAAAACACACGGA

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FIG.1C

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1681 GGTAGAACTATTTCTGTTCCAGTCACATTGCCATCACTCTTGTACTGCCTGCCACCGCG
-----+-----+-----+-----+-----+-----+ 1740
CCATCTTTGATAAAGACAAGGTCAGTGTAAACGGTAGTGAGAACATGACGGACGGTGGCGC

GAGGAGGCTGGTGACAGGCCAAAGGCCAGTGGAAGAAACACCCTTTCATCTCAGAGTCCA
1741 -----+-----+-----+-----+-----+-----+ 1800
CTCCTCCGACCACTGTCCGGTTTCCGGTCACCTTCTTTGTGGGAAAGTAGAGTCTCAGGT

CTGTGGCACTGGCCACCCCTCCCCAGTACAGGGGTGCTGCAGGTGGCAGAGTGAATGTCC
1801 -----+-----+-----+-----+-----+-----+ 1860
GACACCGTGACCGGTGGGGAGGGGTCATGTCCCACGACGTCCACCGTCTCACTTACAGG

CCCATCATGTGGCCCAACTCTCCTGGCCTGGCCATCTCCCTCCCAGAAACAGTGTGCAT
1861 -----+-----+-----+-----+-----+-----+ 1920
GGGTAGTACACCGGTTGAGAGGACCGGACCGGTAGAGGGAGGGGTCTTTGTCACACGTA

GGGTTATTTTGGAGTGTAGGTGACTTGTTTACTCATTGAAGCAGATTTCTGCTTCCTTTT
1921 -----+-----+-----+-----+-----+-----+ 1980
CCCAATAAAACCTCACATCCACTGAACAAATGAGTAACTTCGTCTAAAGACGAAGGAAAA

ATTTTTATAGGAATAGAGGAAGAAATGTCAGATGCGTGCCAGCTCTTCACCCCCCAATC
1981 -----+-----+-----+-----+-----+-----+ 2040
TAAAAATATCCTTATCTCCTTCTTTACAGTCTACGCACGGGTCGAGAAGTGGGGGGTTAG

TCTTGGTGGGGAGGGGTGTACCTAAATATTTATCATATCCTTGCCCTTGAGTGCTTGTTA
2041 -----+-----+-----+-----+-----+-----+ 2100
AGAACCACCCCTCCCCACATGGATTTATAAATAGTATAGGAACGGGAACCTCACGAACAAT

GAGAGAAAGAGAACTACTAAGGAAAATAATATTATTTAAACTCGCTCCTAGTGTTCCTTT
2101 -----+-----+-----+-----+-----+-----+ 2160
CTCTCTTCTCTTGATGATTCCTTTTATTATAATAAATTTGAGCGAGGATCACAAAGAAA

GTGGTCTGTGTCACCGTATCTCAGGAAGTCCAGCCACTTGACTGGCACACACCCCTCCGG
2161 -----+-----+-----+-----+-----+-----+ 2220
CACCAGACACAGTGGCATAGAGTCCTTCAGGTCGGTGAACCTGACCGTGTGTGGGGAGGCC

ACATCCAGCGTGACGGAGCCCACTGCCACCTTGTTGGCCGCCTGAGACCCTCGCGCCCC
2221 -----+-----+-----+-----+-----+-----+ 2280
TGTAGGTCGCACTGCCTCGGGTGTGACGGTGGAACACCGGCGGACTCTGGGAGCGCGGGG

CCGCGCCCCCGCGCCCCCTCTTTTCCCCTTGATGGAAATTGACCATACAATTTATCCT
2281 -----+-----+-----+-----+-----+-----+ 2340
GGCGCGGGGGGCGCGGGGAGAAAAAGGGGAACCTTTAACTGGTATGTTAAAGTAGGA

FIG. 1D

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2341 CCTTCAGGGGATCAAAAGGACGGAGTGGGGGGACAGAGACTCAGATGAGGACAGAGTGGT
-----+-----+-----+-----+-----+-----+ 2400
GGAAGTCCCCTAGTTTTCTGCCTACCCCCCTGTCTCTGAGTCTACTCCTGTCTCACCA

2401 TTCCAATGTGTTCAATAGATTTAGGAGCAGAAATGCAAGGGGCTGCATGACCTACCAGGA
-----+-----+-----+-----+-----+-----+ 2460
AAGGTTACACAAGTTATCTAAATCCTCGTCTTTACGTTCCCCGACGTACTGGATGGTCCT

2461 CAGAACTTTCCCAATTACAGGGTGACTCACAGCCGATTGGTGACTCACTTCAATGTGT
-----+-----+-----+-----+-----+-----+ 2520
GTCTTGAAAGGGGTTAATGTCCCACTGAGTGTGCGCGTAACCACTGAGTGAAGTTACACA

2521 CATTTCCGGCTGCTGTGTGTGAGCAGTGGACACGTGAGGGGGGGTGGGTGAGAGAGACA
-----+-----+-----+-----+-----+-----+ 2580
GTAAAGGCCGACGACACACTCGTCACCTGTGCACTCCCCCCCCACCACTCTCTCTGT

2581 GGCAGCTCGGATTCAACTACCTTAGATAATATTTCTGAAAACCTACCAGCCAGAGGGTAG
-----+-----+-----+-----+-----+-----+ 2640
CCGTGCGACCTAAGTTGATGGAATCTATTATAAAGACTTTTGGATGGTCGGTCTCCCATC

2641 GGCACAAAGATGGATGTAATGCACTTTGGGAGGCCAAGGCCGGGAGGATTGCTTGAGCCCA
-----+-----+-----+-----+-----+-----+ 2700
CCGTGTTTCTACCTACATTACGTGAAACCTCCGGTTCCGCCCTCCTAACGAACTCGGGT

2701 GGAGTTCAAGACCAGCCTGGGCAACATACCAAGACCCCCGTCTCTTTAAAAATATATATA
-----+-----+-----+-----+-----+-----+ 2760
CCTCAAGTTCTGGTCGGACCCGTTGTATGGTTCTGGGGCAGAGAAATTTTATATATAT

2761 TTTTAAATATACTTAAATATATATTTCTAATATCTTTAAATATATATATATATTTTAAAG
-----+-----+-----+-----+-----+-----+ 2820
AAAATTTATATGAATTTATATATAAAGATTATAGAAATTTATATATATATATAAAATTC

2821 ACCAATTTATGGGAGAATTGCACACAGATGTGAAATGAATGTAATCTAATAGAAGC
-----+-----+-----+-----+-----+-----+ 2876
TGGTTAAATACCCTCTTAACGTGTGTCTACACTTTACTTACATTAGATTATCTTCG

FIG. 1E

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MQMSPALTCLVLGLALVFGECSA
Signal Peptide

VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVFSPYGVASVLAMLQLTTGGETQQQIQA
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTDAIFVQRDLKLVGFMPPHFFRLFRST
VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP
DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDLSMFIAAP
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR
QFQADFTSLSDQEPLHVAQALQVKVIEVNESGTVASSSTAVIVSARMAPEEIMDRPFLF
VVRHNPTGTVLFMGQVMEP

FIG.2A

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10	20	30	40	50	60
VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSYGVASVLAMLQLTTGGETQQQIQ					
70	80	90	100	110	120
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPPHFFRLFRST					
130	140	150	160	170	180
VKQVDFSEVERARFIINDWVKHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP					
190	200	210	220	230	240
DSSTHRRLFHKSDGSTVSPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAP					
250	260	270	280	290	300
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR					
310	320	330	340	350	360
QFQADFTSLSDQEPLHVAQALQVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLF					
370					
VVRHNPTGTVLFMGQVMEP					

FIG.2B

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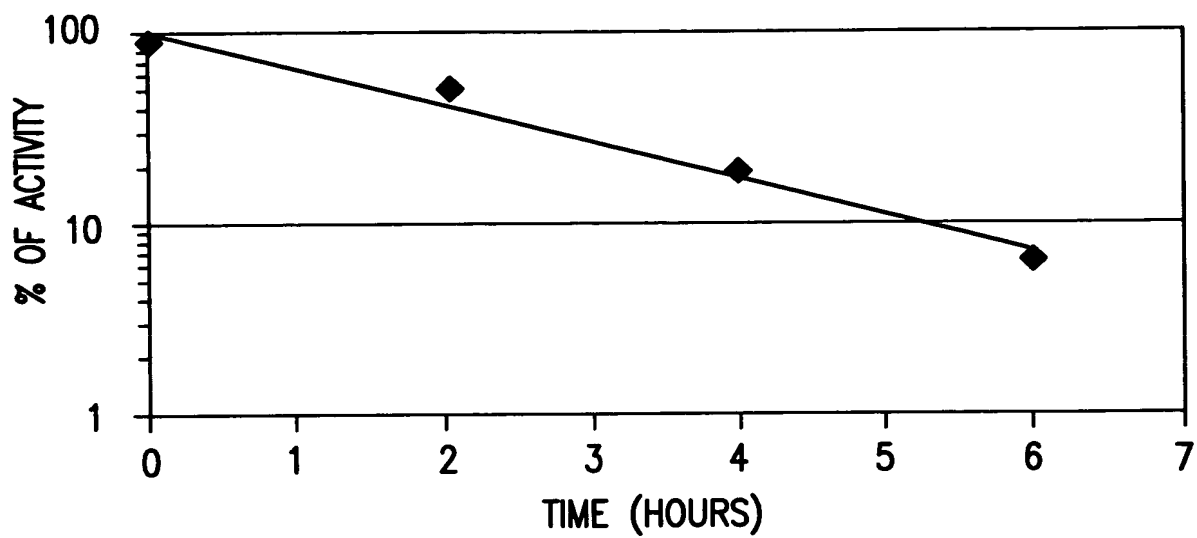


FIG.3

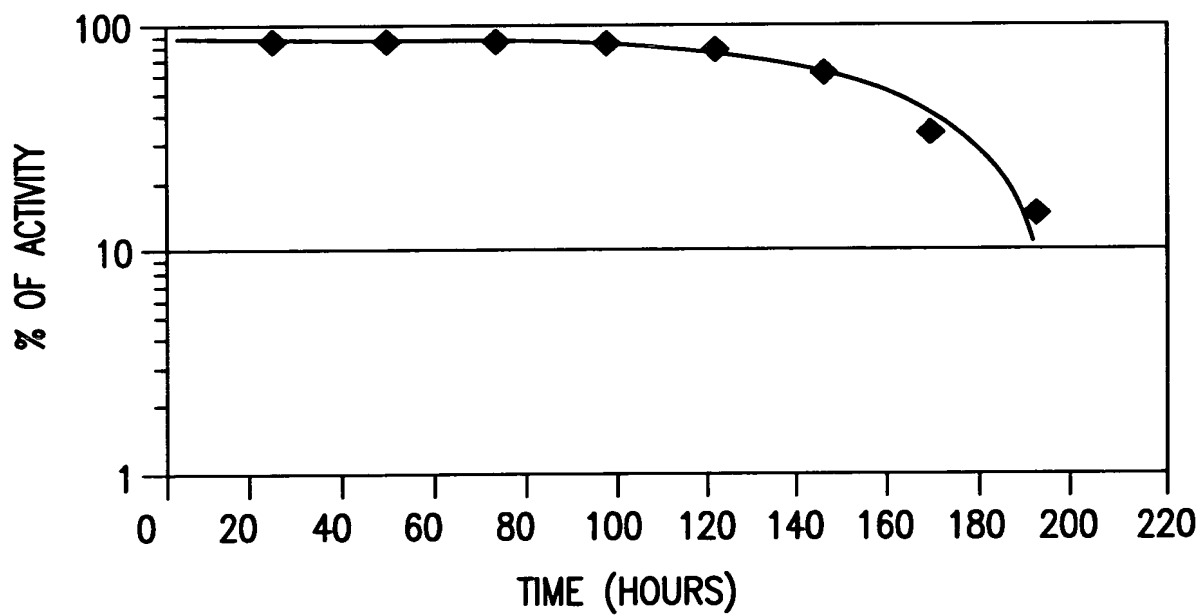


FIG.4

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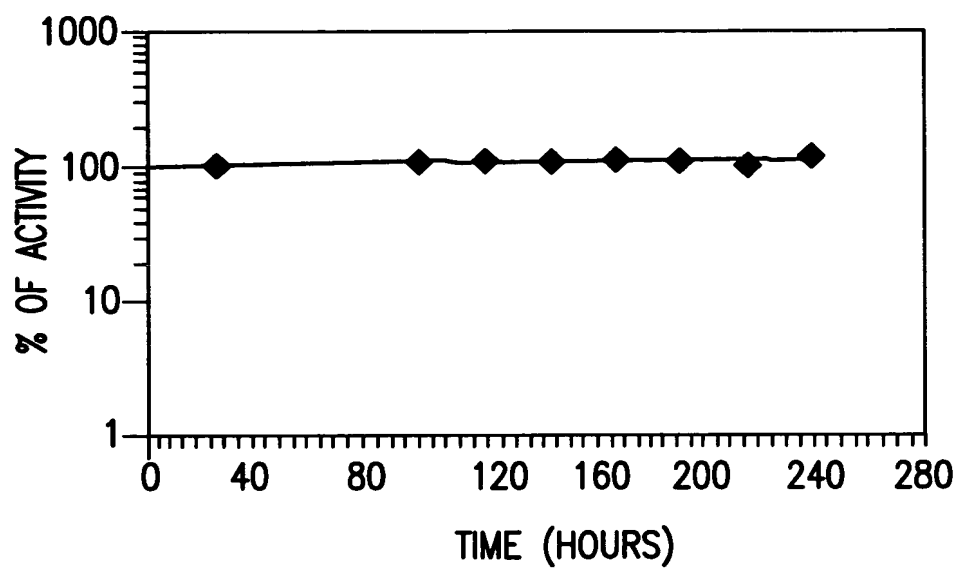


FIG.5

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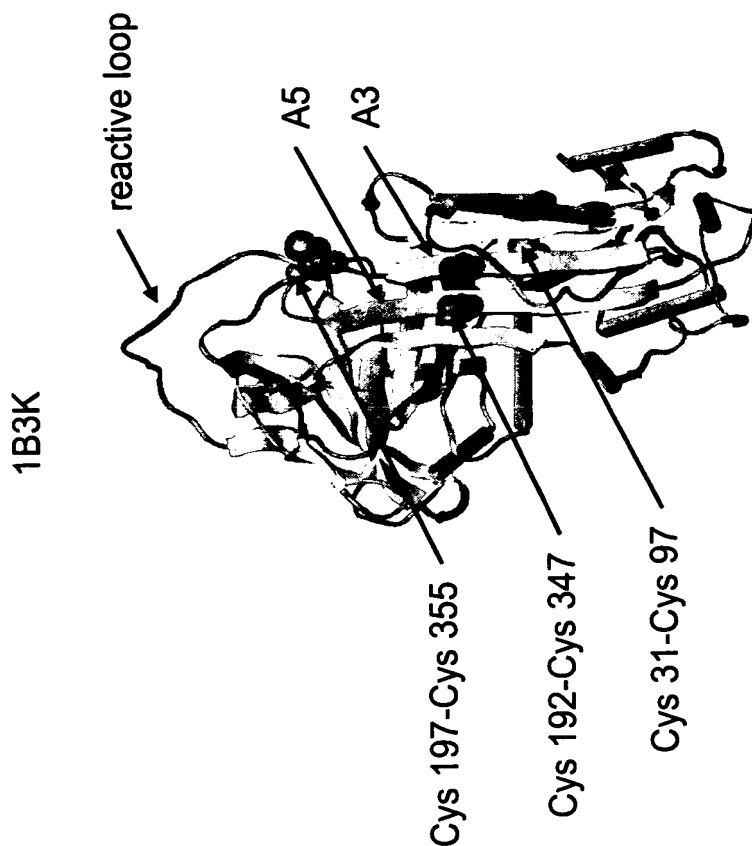


FIG. 6B

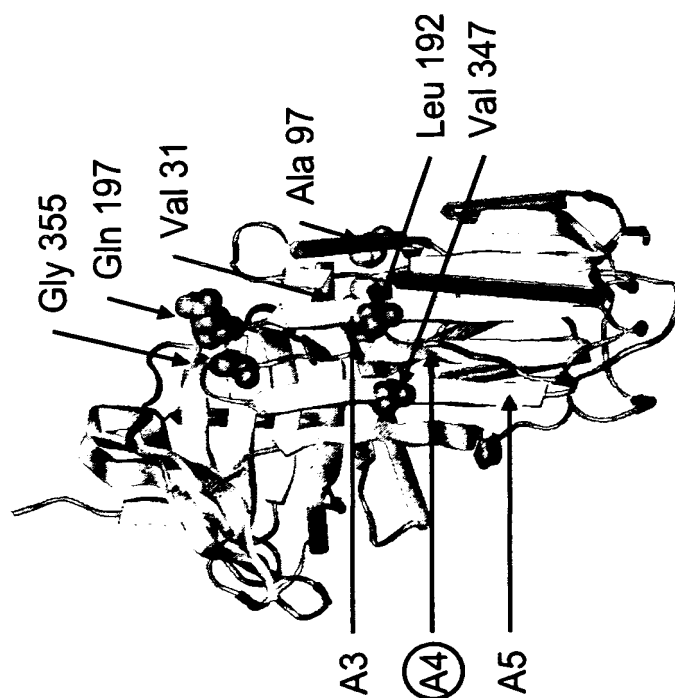


FIG. 6A

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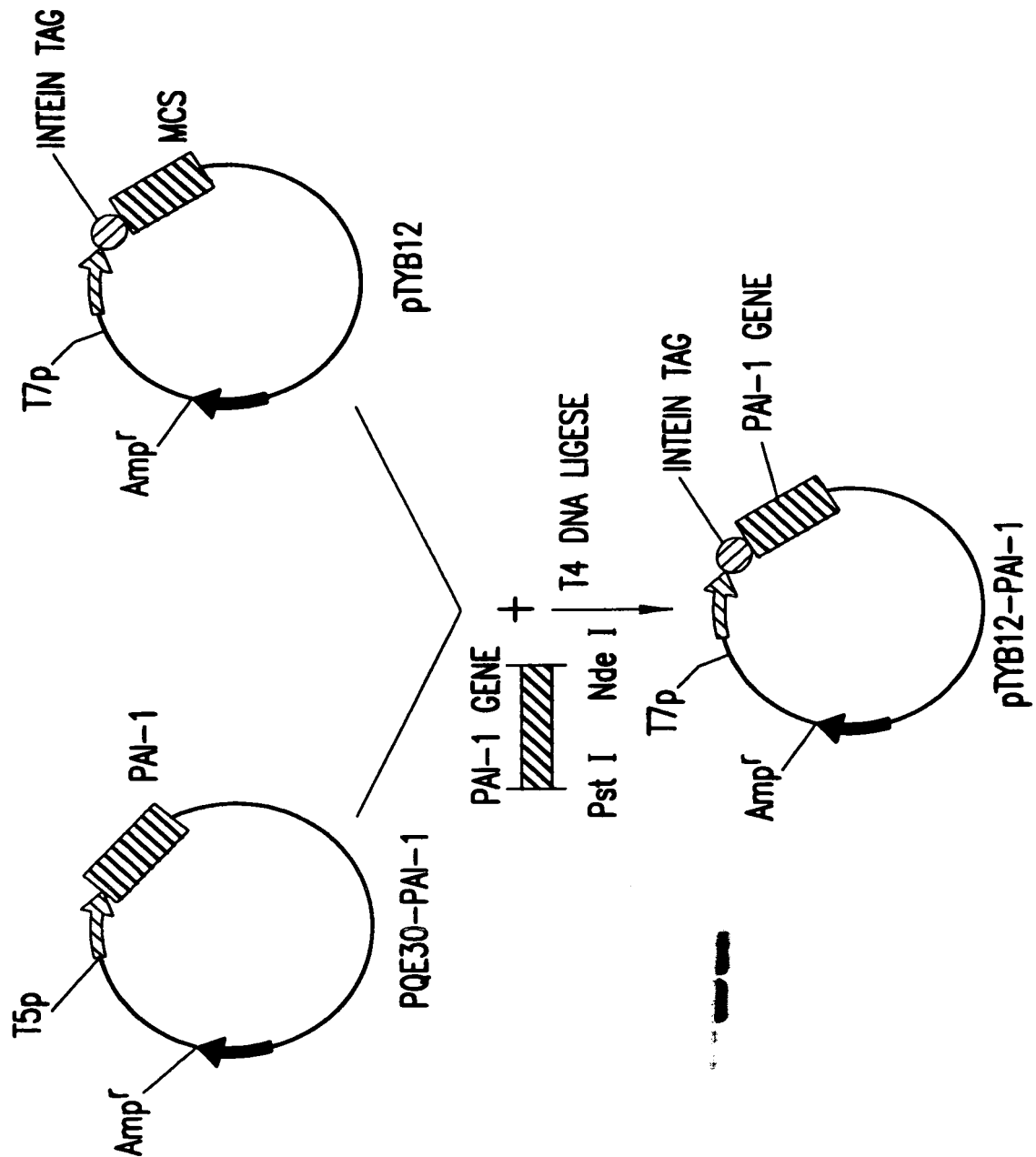


FIG.7

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FIG. 8A

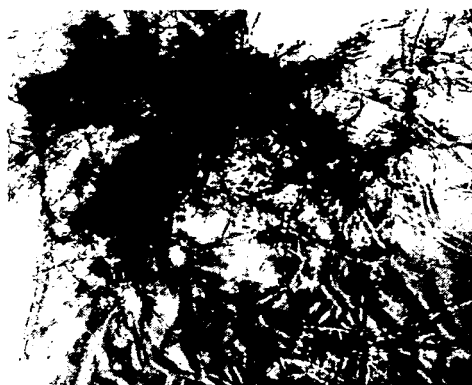


FIG. 8B

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FIG. 9A



FIG. 9B

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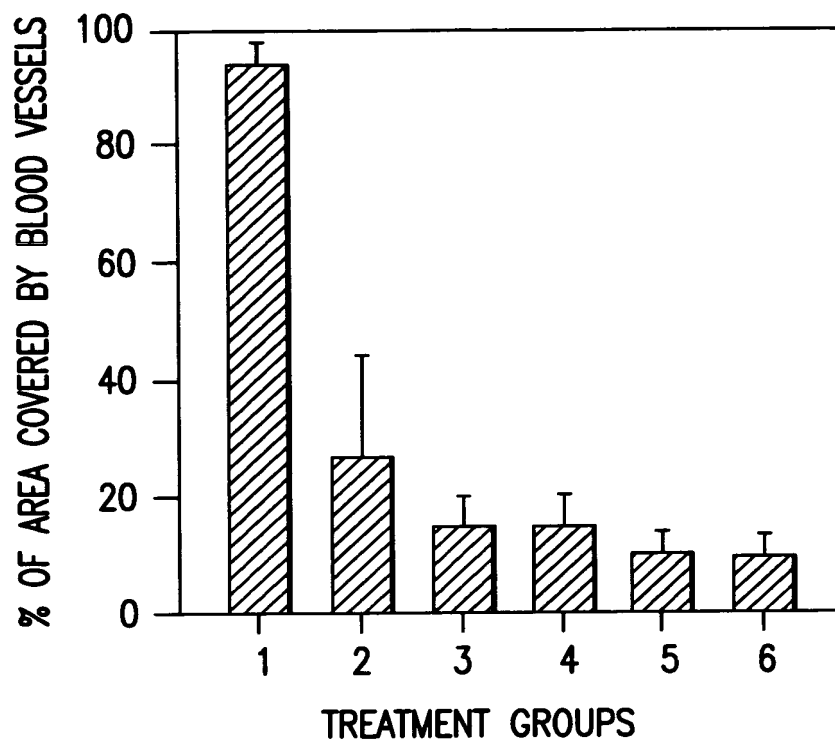


FIG.10

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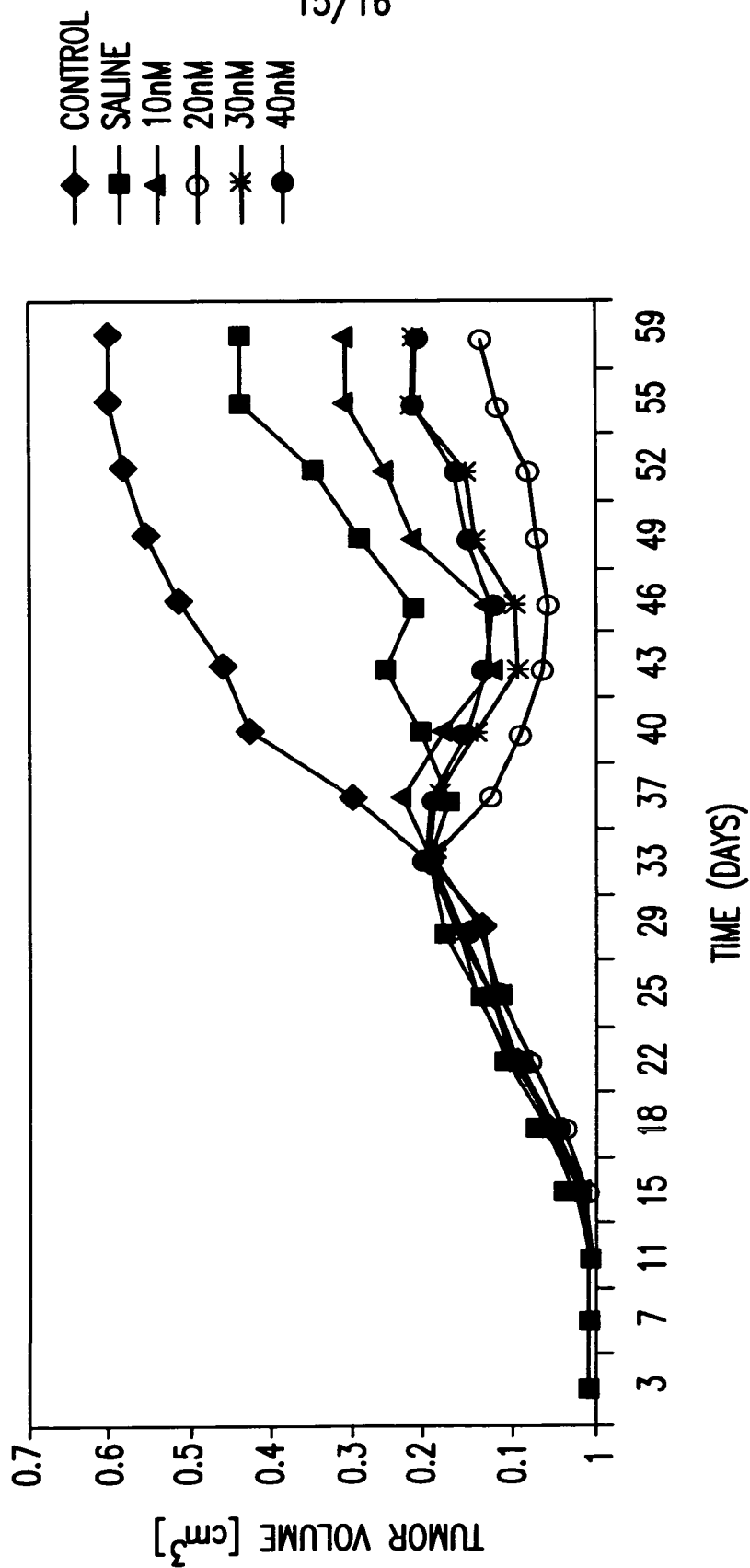


FIG.11

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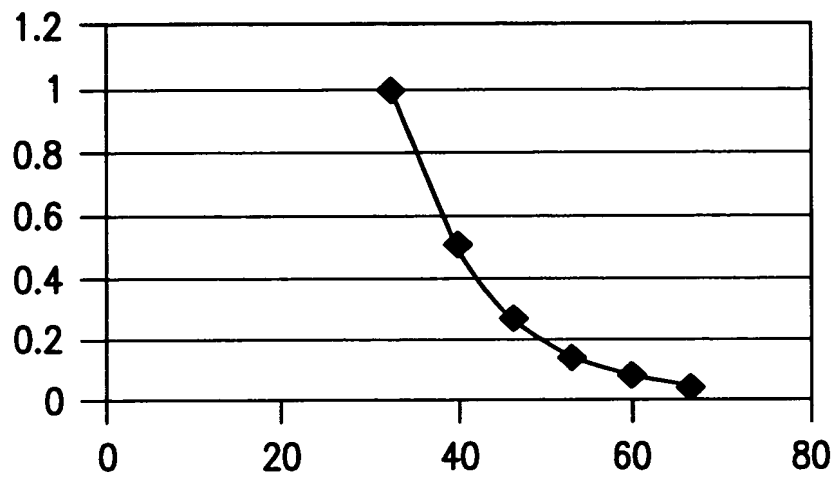


FIG.12